

Estimated of Genetic Parameters for Time on Test and Backfat Thickness for Gilts from Field Test

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SUMMARY

In year 2003, experimental genetic evaluation with BLUP was implemented for fattening traits in gilts in Croatia. Pure- and cross- bred animals were included. Slovenian information system PiggyBank was adapted. Strong emphasis was done on data quality. Two main problems were small number of data and inaccurate measurements of body weight and backfat in gilts. Consequently, estimated genetic parameters were improper for genetic evaluation. Better measurements and more data will lead to better estimations of dispersion parameters. Genetic evaluation for litter size, analyses of phenotypic and genetic trends are planed in the future.

KEY WORDS

BLUP, pigs, information system, genetic evaluation

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INTRODUCTION

Number of pigs in year 2002 in Croatia was 185 000 (Croatian Bureau of Statistics, 2002). Croatian nucleus and reproduction farms are located on ten large farms. Family farms are small units, with average herd size from 3 to 20 sows (Croatian Livestock Selection Center, 2003). Pig breeding program is based on static three- and four-cross breeding scheme with Swedish, German Landrace and Large White as dam breeds and Pietrain and Duroc as sire breeds. In year 2002, 1637 boars (station and field test) and 4678 gilts (field test) were tested. Data from family and large farms is stored in Croatian Livestock Center (CLC) database. In year 2003, 30073 sows were recorded (Croatian Livestock Selection Center, 2003). CLC has 27 regional offices around the country. Regional offices collect data from field test of gilts and boars on family farms. Data is transferred to the central CLC database in Zagreb. Large farms have locally installed computers and organize data collection (station and field test) themselves.

Nowadays, Best Linear Unbiased Prediction – BLUP (Henderson, 1984) is standard for prediction of breeding values. Before BLUP can be applied, phenotypic and genetic parameters had to be estimated. Restricted Maximum Likelihood – REML (Patterson and Thompson, 1971) is a method of choice for this task. The aim of this paper was to estimate phenotypic and genetic parameters for time on test and backfat thickness for gilts from field test.

MATERIAL AND METHODS

Gilts are tested for time on test (TL) and ultrasonic backfat thickness (BF). Time on test represents days from birth to average weight at the end of test, which is 105 kg. They are housed in groups. Before measurements are taken, gilts are usually selected on the basis of condition score. Data from field test, collected between January 1996 and December 2002 at six large farms were analyzed. Only Swedish (SL) and German Landrace (GL), Large White (LW), Pietrain (PI), and crossbreeds SL x LW, LW x SL and GL x LW were included. Data (576 records) from first years of field testing were excluded, because number of records was small within farm and year.

Additionally, 8837 had to be excluded, because of insufficient quality. Most of those records had body weight 100 kg and backfat thickness 10 mm. Gilts weighing less than 70 and more than 130 kg were also excluded. After cleaning of data, 12034 recorded gilts and 17989 animals from pedigree (Table 1) were included on the analysis.

At the end of the test gilts had on average body weight 106.4 kg, and 11.12 mm of backfat (Table 2). The average time on test was 201.1 days. There were not large differences between farms in average body weight and backfat thickness, only farm C (Table 2) had higher body weight (120.58 kg) and backfat thickness (14.20 mm). Time on test was more variable between farms.

Models for genetic evaluation can be written in scalar notation as following:

$$y_{ijkl} = \mu + S_i + G_j + b_j (x_{ijkl} - \bar{x}) + l_{jk} + a_{ijkl} + e_{ijkl}$$

$$y_{2ijkl} = \mu + S_i + G_j + l_{jk} + a_{ijkl} + e_{ijkl}$$

where y_{ijkl} is ultrasonic backfat thickness as average of three measurements (mm), y_{2ijkl} is age at the end of test, μ the overall mean, S_i (year-month interaction) and G_j are fixed effects of season and breed, x_{ijkl} is body weight at the end of test, l_{jk} are random effects of common litter environment, a_{ijkl} is direct additive genetic effect (breeding value) and e_{ijkl} residual.

These two models were used in bivariate analysis. The bivariate model can be presented in matrix notation as following:

$$y = X\beta + Z_l l + Z_a a + e$$

Where y represents the observation vector (time on test and backfat thickness), β vector of unknown parameters for fixed effects, l vector of common litter environmental effect, a vector of animal genetic effect (breeding values) and e vector of residual. Matrices X , Z_l , Z_a , are corresponding incidence matrices. Expectations and covariance matrices of random variables are described in [1], where A is additive genetic relationship matrix and L_o , G_o and R_{ko} present (co)variance components.

Table 1. Data and pedigree structure by farm

Farm	Data	Pedigree	No. sires	No. dams	No. base animals
A	1799	2939	130	1023	543
B	534	947	98	327	134
C	416	1172	64	479	207
D	1762	2287	78	681	377
E	6929	9782	323	3212	816
F	594	862	41	257	137
Total	12034	17989	734	5975	2214

Table 2. Descriptive statistics for body weight, backfat thickness and time on test by farm

Farm	Body weight (kg)		Time on test (days)		Backfat thickness (mm)	
	\bar{x}	SD	\bar{x}	SD	\bar{x}	SD
A	112.5	10.48	206.7	20.22	11.66	2.16
B	103.3	4.09	188.9	12.23	9.76	1.23
C	120.6	11.85	260.9	24.49	14.20	3.26
D	102.5	3.46	199.8	9.15	10.25	1.14
E	105.0	11.12	199.4	13.77	11.08	1.39
F	105.2	7.49	186.3	21.15	10.97	1.84
Total	106.4	10.79	201.1	19.25	11.12	1.79

$$E \begin{bmatrix} y \\ l \\ a \\ e \end{bmatrix} = \begin{bmatrix} X\beta \\ 0 \\ 0 \\ 0 \end{bmatrix} \quad V \begin{bmatrix} l \\ a \\ e \end{bmatrix} = \begin{bmatrix} I \otimes L_0 & 0 & 0 \\ 0 & A \otimes G_0 & 0 \\ 0 & 0 & \sum_{i=1}^n \otimes R_{ko} \end{bmatrix} [1]$$

Fixed part of the model was developed with SAS package (SAS, 2001). Estimation of covariance components was based on REML method using the VCE-5 software package (Kovač and Groeneveld, 2002). PEST program (Groeneveld et al., 1990) was used for prediction of breeding values.

RESULTS

Data quality

During data checking and validation following errors were found: doubled records for farrowing, weaning and insemination, repeated animal identification in same breed, active animals where recorded as culled, abortions where not recorded etc. Frequency of measured gilts was very high at weights 100 and 110 kg (Figure 1a) indicating that weighing was not precise. Similar situation was for backfat thickness, where the most frequent value was 10-12 mm (Figure 1b), but varied between farms.

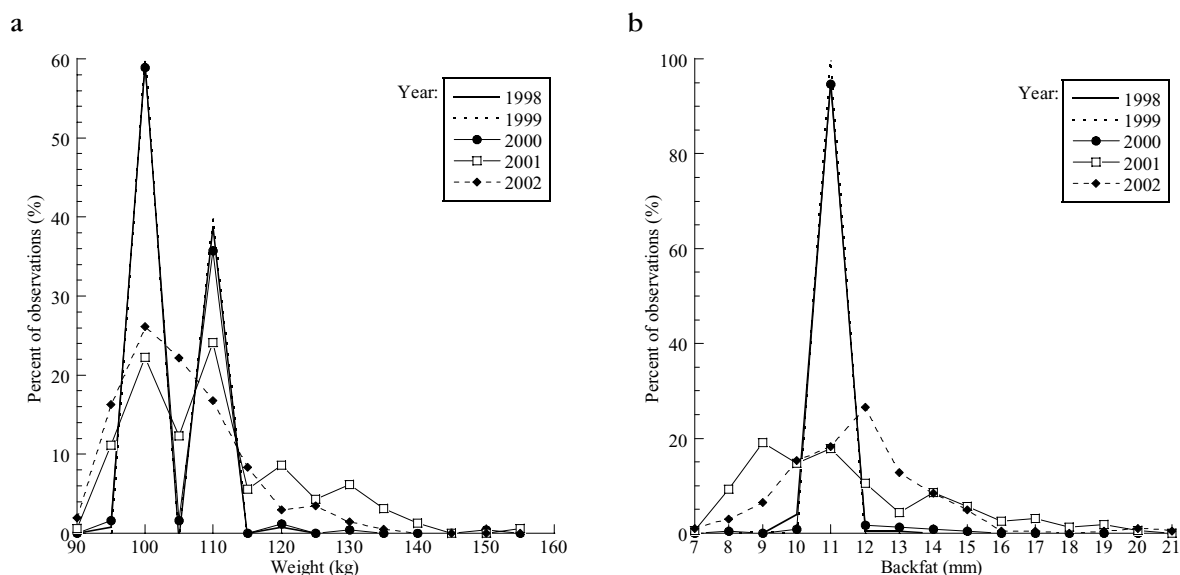


Figure 1. Distribution of body weight and backfat on farm F

Estimates of dispersion parameters

Genetic analyses were performed separately for each farm (Table 3). Phenotypic variances for time on test varied between 45.32 day² for farm D up to 323.14 day² for farm C, which was seven times higher compared to farm D. Minimum (0.42 mm²) and maximum (8.79 mm²) for backfat thickness were achieved on the same two farms. The estimated heritability ranged between 0.002 and 0.35 for time on test in separate analysis. A similar situation was found for backfat where combined heritability accounted for 0.52 compared to range between 0.01 and 0.30 for farms. Genetic correlation between time on test and backfat thickness differed from - 1.00 up to 0.70 (Table 4).

DISCUSSION

Since there is no unique registration system for pigs in Croatia, and with the purpose of creating valid pig database, unique lifetime number had to be assured for each animal in the system. The information system was reorganized. Data are in procedure of cleaning by correcting or deleting mistakes. Second problem represents small number of measured animals.

Table 3. Estimates of phenotypic variance (V_p) and ratios for common litter environmental and additive genetic effect for time on test (TL) and backfat thickness (BF)

Farm	Phenotypic variance (V_p)		Litter (I^2)		Animal (h^2)	
	TL	BF	TL	BF	TL	BF
A	196.38	3.83	0.13	0.19	0.23	0.25
B	85.60	1.33	0.25	0.13	0.002	0.01
C	323.14	8.79	0.06	0.10	0.35	0.30
D	45.32	0.42	0.18	0.07	0.12	0.02
E	121.32	0.74	0.20	0.19	0.05	0.04
F	284.34	2.88	0.40	0.12	0.16	0.29

Table 4. The correlations between time on test and backfat thickness for common litter environmental and additive genetic effect

Farm	Litter	Animal
A	-0.06	0.15
B	0.87	-1.00
C	-0.27	0.70
D	0.55	-0.15
E	0.14	0.34
F	0.40	0.33

Prediction of breeding values with BLUP uses all possible information from relatives, however reliable predictions demand measurements and appropriate size of contemporary groups. Sophisticated methods for prediction have no sense if traits are measurement imprecise. With better measurements and more data, estimations of dispersion parameters are expected to be trustworthy for use in breeding value prediction. Imprecise measurements and small amount of data are reasons for narrow distribution of breeding values, too.

Heritability estimates on farm B were negligible most probably due to small size of the dataset which contained only 9.7 offspring per sire and 2.9 per dam. In addition, the standard deviation for both traits as well as independent variable body weight was very low. Low variation was observed also on farm D which has a better structure of the data: the dataset is 3.3 times larger, 22.6 offspring per sire, and 2.6 offspring per dam. Nevertheless, heritability estimates were low. A good data structure is observed for farm E, however heritability estimated were too low as well. Contrary, the other farms had better variation and independently of the data size, the estimates were comparable to Slovenian estimates where field test is carried under similar conditions (unpublished). Low estimates on some farms may be due to low data quality. The data were collected and not used for selection as well as management reducing interest of the breeder. It is expected that new records will be of better quality. Ratios for common litter effects are slightly higher than the estimates in Slovenia. Nevertheless, they are closer to expected values

than heritability estimates. Correlation coefficients between time on test and backfat thickness varied quite a lot (Table 4), from -1.00 to 0.70 for genetic effect and from -0.27 to 0.87 for common litter environmental effect. The range is too wide to rely on them. In Slovenia, genetic as well as litter correlations were small and negative. Besides data quality, the sizes of the datasets are even more crucial for correlations as for variance ratios.

CONCLUSION

Croatian Livestock Center does not have necessary software and experience with implementing BLUP, and first steps will be made in cooperation of Biotechnical Faculty from Slovenia.

Slovenian information system PiggyBank was adapted, and procedure of data handling is under trial. Temporary data quality is insufficient, and need to be improved.

The existing data should be available to different applications, and any new data should be easily incorporated into the existing data base structure.

Optimal model was set up for genetic evaluation of fattening traits in gilts, and dispersion parameters were estimated. Variance components and prediction of breeding values are unreliable at this moment.

Genetic evaluation for litter size, analyses of phenotypic and genetic trends are planed in the future.

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